

Figure 1

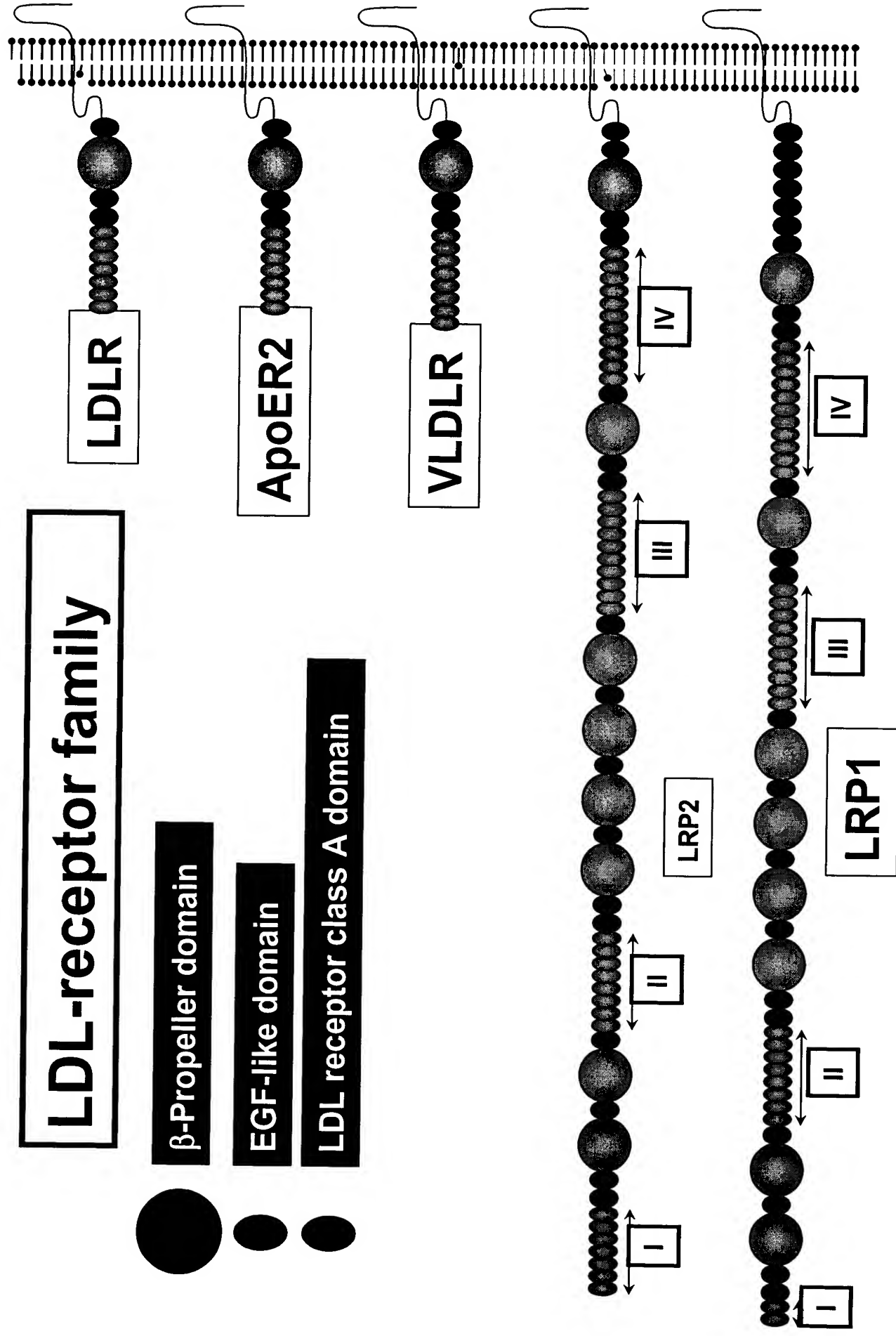


Figure 2

## LDL-receptor class A domain

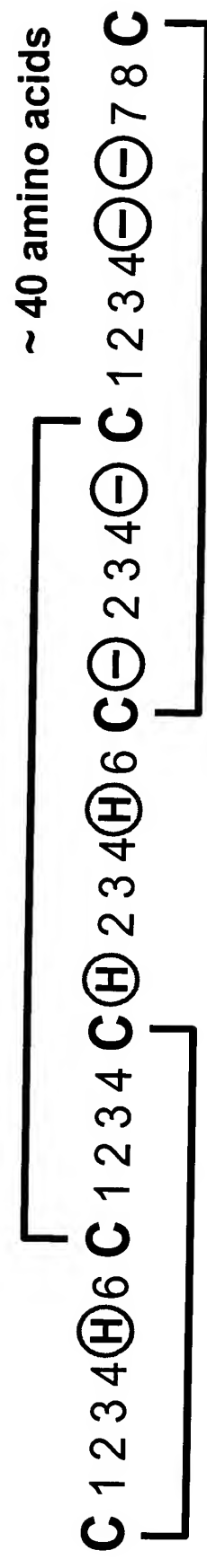
LRP1_HUMAN	C.EPYQFRCKNNR.....CVPGRWQ.CDYDNDCGDNSDEES.....C
LRP1_HUMAN	C.LPSQFKCTNTNR.....CIPGIFR.CNGQDNCGDGEDERD.....C
LDLR_HUMAN	C.SQDEFRCHDGK.....CISRQFV.CDSDRDCLDGSDEAS.....C
LRP2_HUMAN	C.SSSAFTCGHGE.....CIPAHWR.CDKRNDCVDGSDEHN.....C
LRP2_HUMAN	C.SSSEFQCASGR.....CIPQHWY.CDQETDCFDASDEPAS....C
CORI_HUMAN	CHSQGLVECRNGQ.....CIPSTFQ.CDGDEDCCKDGSDEEN.....C
MAT_HUMAN	C.PAQTFRCSNGK.....CLSKSQQ.CNGKDDCGDGSDEAS.....C
CO8B_HUMAN	C...EGFVCAQTGR.....CVNRRLL.CNGDNDCGDQSDEAN.....C
MAT_HUMAN	C.TKHTYRCLNGL.....CLSKGNPECDGKEDCSDGSDEKD.....C
LDVR_HUMAN	CLGPGKFKCRSGE.....CIDISKV.CNQEQDCRDWSDEPLKE..C
APOER2_HUM	C.PAEKLSCGPTSHK...CVPASWR.CDGEKDCEGGADEAG.....C
SORL_HUMAN	CTHFMDFVCKNRQQ.....CLFHSMV.CDGIIQCRDGSDEDAAFAGC
ST7_HUMAN	C.AYNQFQCLSRFTKVYTCLPESLK.CDGNIDCLDLGDEID.....C
consensus	C.1234F6C12G4.....CI23456.CDG34DC1D3SDE78.....C

FIGURE 3

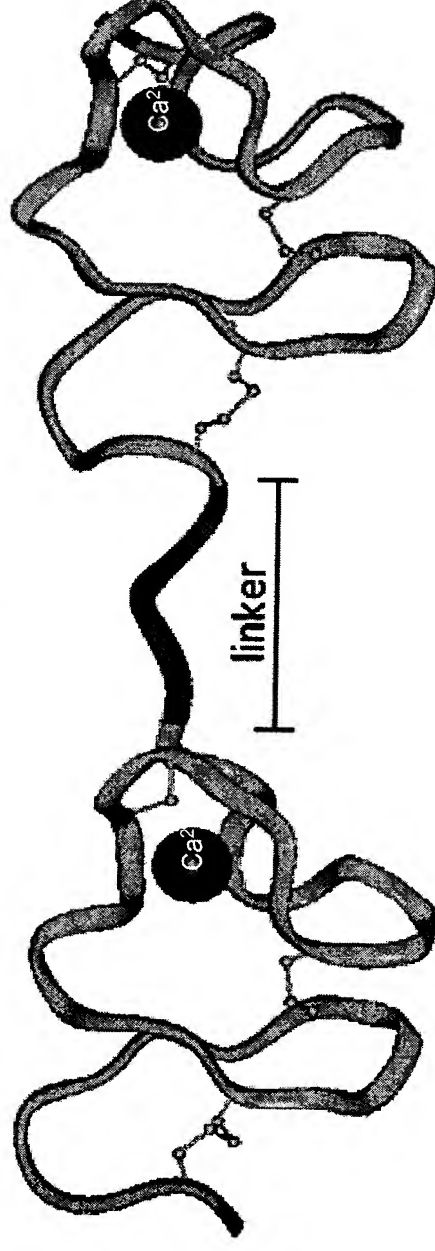
# A-domains

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A



B



# Figure 4

## Ligands recognized by LDL-receptor family

<i>proteases</i>	<i>proteins involved in</i>	<i>miscellaneous</i>
factor IXa	<i>lipoprotein metabolism</i>	albumin
pro-uPA	apoB100	transthyretin
t-PA	apoE	$\beta$ -Amyloid precursor protein
plasminogen	apoJ (clusterin)	RAP
MMP-9	apoH ( $\beta_2$ -glycoprotein I)	complement C3
	Lp(a)	lactoferrin
<i>inhibitors</i>	hepatic lipase	thyroglobulin
$\alpha_2$ -macroglobulin	lipoprotein lipase	thrombospondin
PAI-1	IDL	saposin precursor
TFPI	VLDL	reelin
pancreatic trypsin inhibitor	$\beta$ -VLDL	insulin
		parathyroid hormone (PTH)
<i>complexes</i>	<i>non-human</i>	aprotinin
protease/	pseudomonas exotoxin A	$\alpha$ -amylase
$\alpha_1$ -antitrypsin	circumsporozoite protein	C1q
protein C inhibitor	trichosanthin	$\alpha_1$ -microglobulin
protease nexin-1	ricin A	$\beta_2$ -microglobulin
antithrombin	saporin	odorant-binding protein
C1-inhibitor	<i>antibiotics</i>	epidermal growth factor
thrombin/heparin cofactor II	gentamicin	prolactin
cathepsin G/ $\alpha_1$ -antichymotrypsin	polymyxin B	lysozyme
	<i>viruses</i>	connective tissue growth factor (CTGF)
<i>vitamin-carrier complexes</i>	HRV2 (Rhino)	cytochrome c
vitamin D-bp, vitamin D	HCV (Flavi)	seminal vesicle secretory protein II
retinol-bp, vitamin A	BVDV (Flavi)	clara cell secretory protein (CCSP)
transcobalamin, vitamin B12		cubulin
		factor VIII

Figure 5

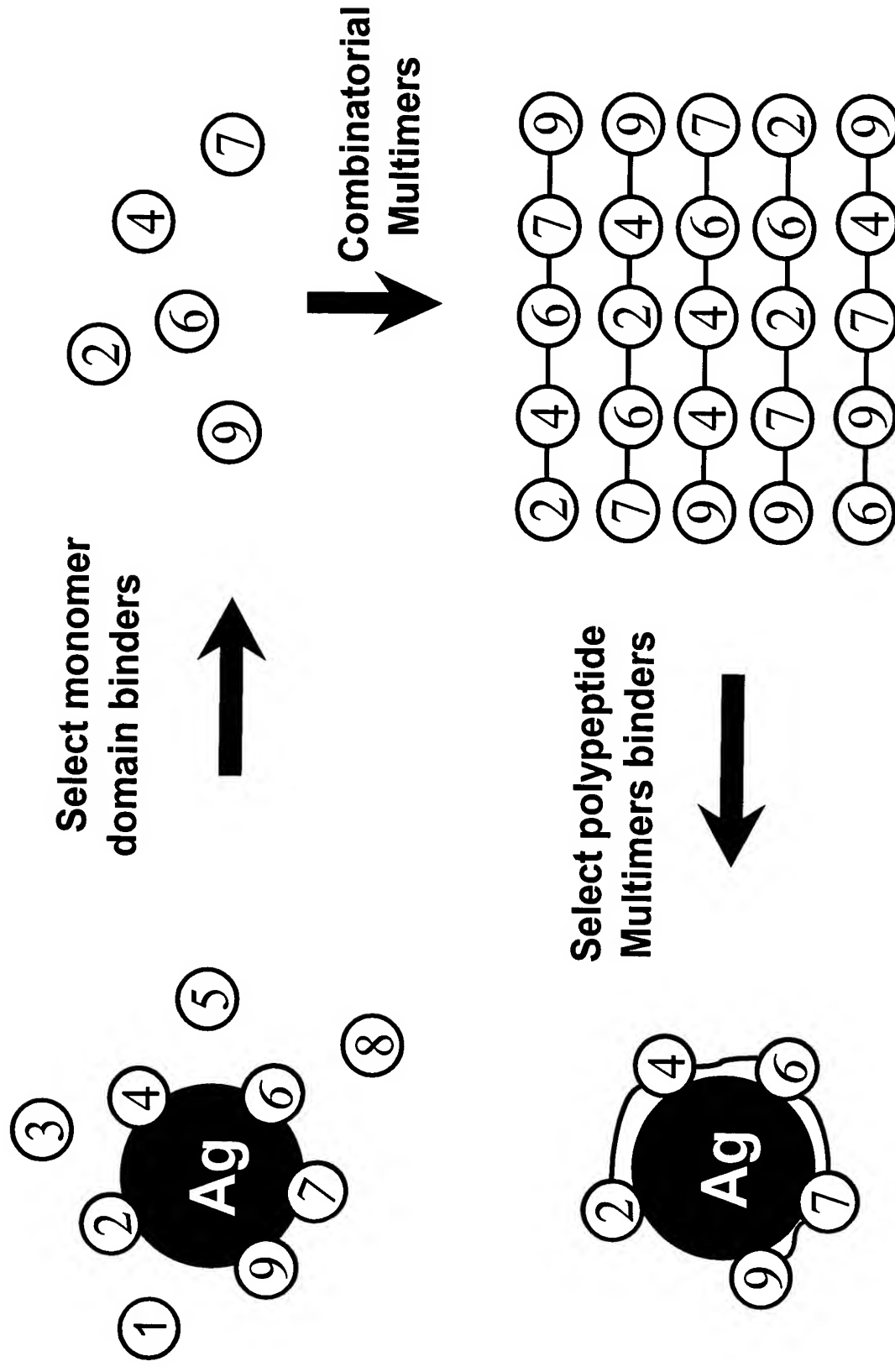


Figure 6

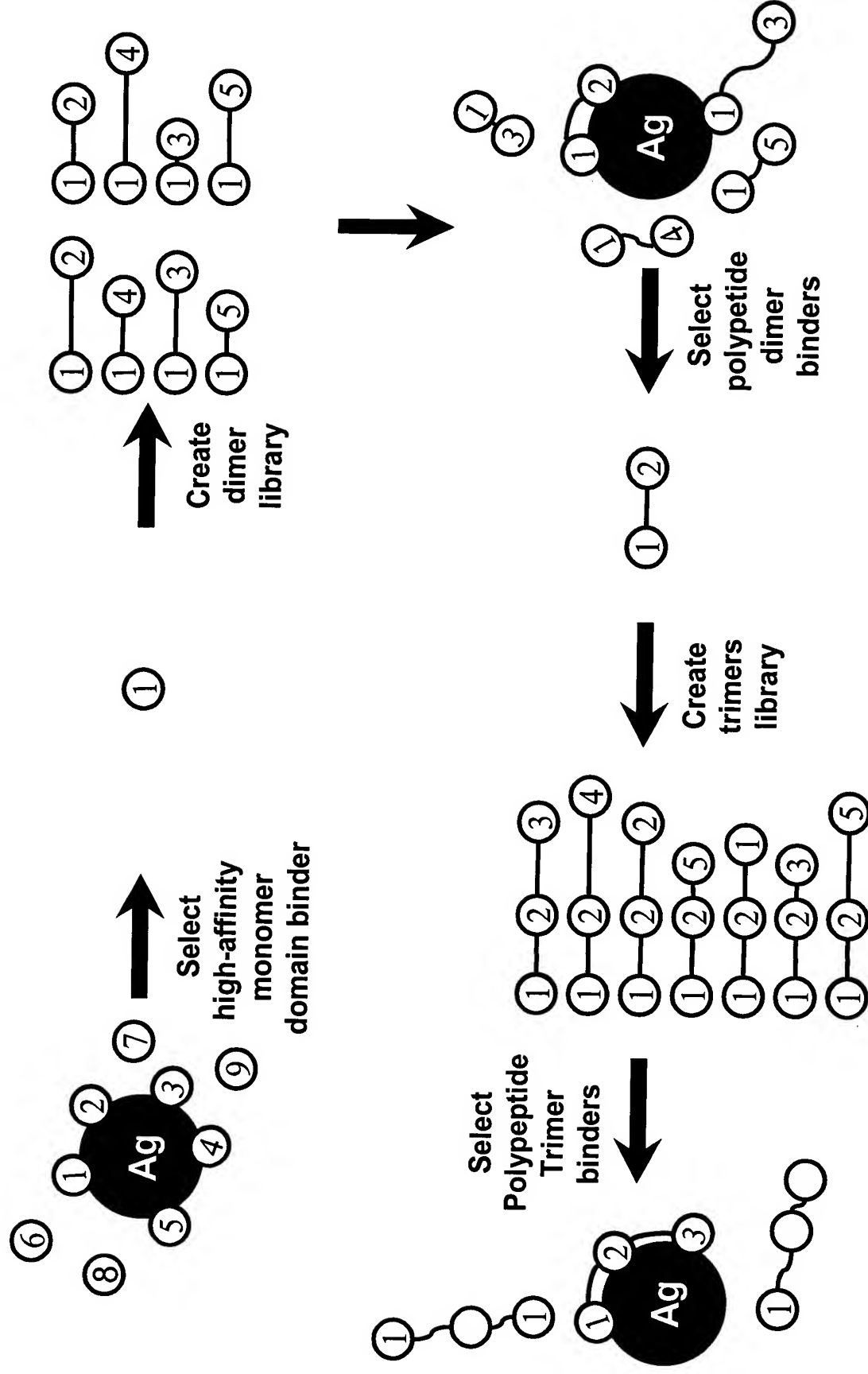


Figure 7

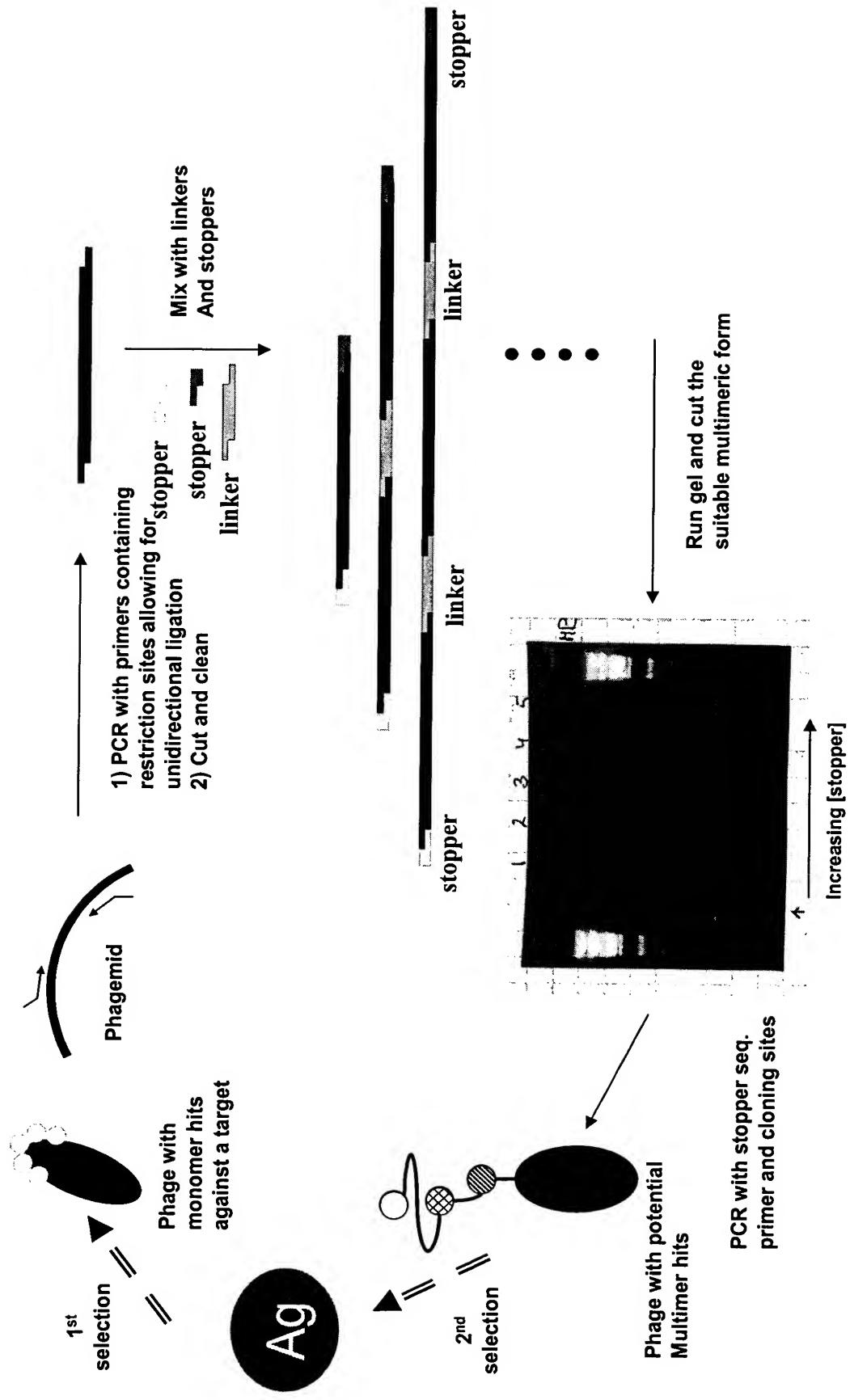


Figure 8

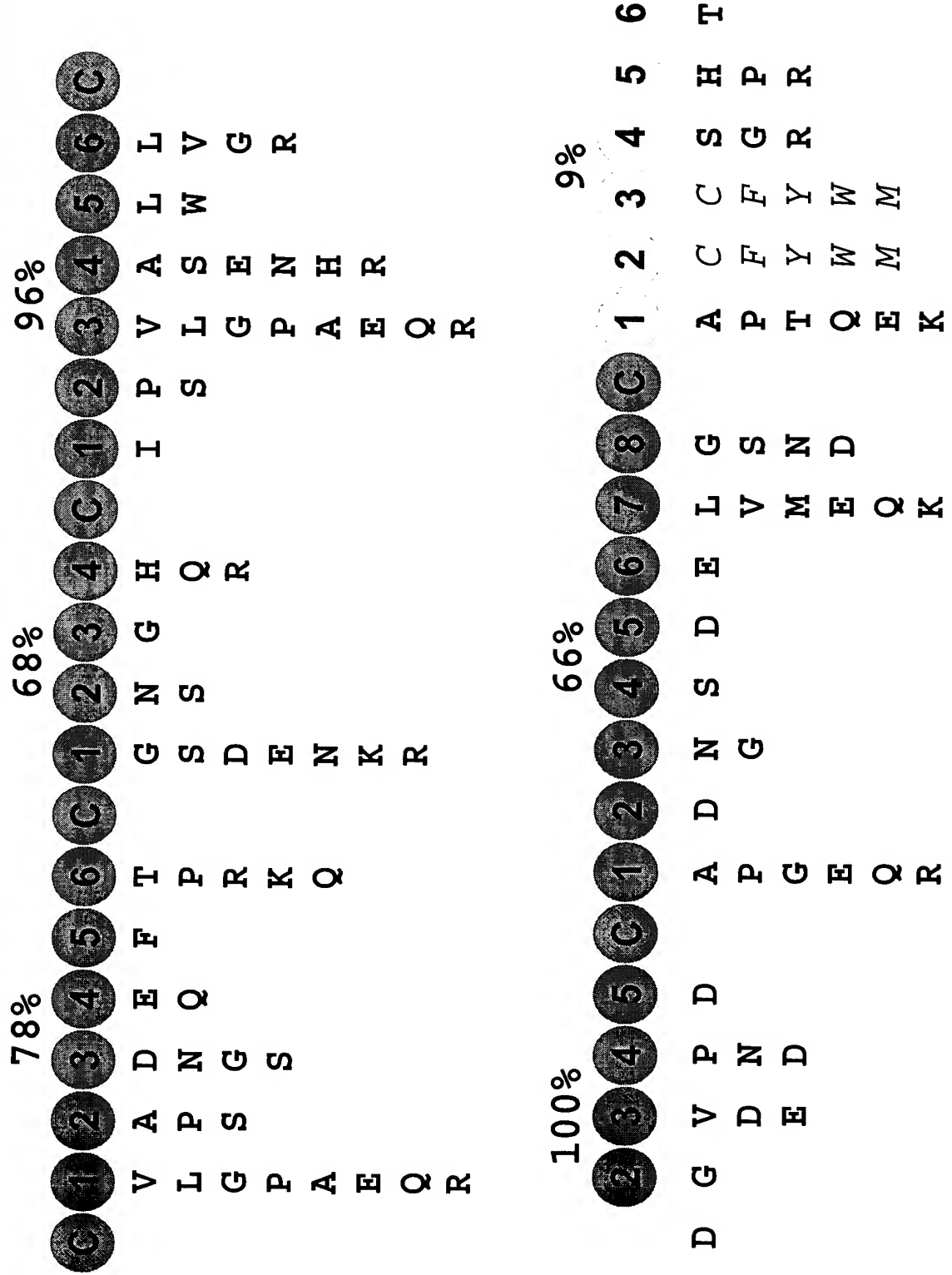




FIG. 9A

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
A	0.0	<u>7.1</u>	12.3	3.2	1.9	1.9	7.1	0.0	15.8	1.5	0.0	1.5	0.0	1.0	3.7	7.3	9.4
C	100.0	0.0	0.6	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	1.5	99.5	0.0	0.0	0.0	0.0
D	0.0	5.2	4.5	19.5	2.6	0.0	0.0	0.0	8.3	<u>10.5</u>	2.3	0.8	0.0	0.0	3.7	1.6	4.7
E	0.0	4.5	9.7	2.6	37.0	0.0	3.9	0.0	3.8	0.0	0.8	9.8	0.0	0.0	1.6	7.3	7.3
F	0.0	0.6	0.0	3.9	1.9	76.0	0.6	0.0	0.8	0.0	0.0	0.8	0.0	0.5	1.6	2.1	2.6
G	0.0	13.0	3.2	16.2	1.9	0.0	0.0	0.0	12.8	0.8	72.2	2.3	0.0	0.0	3.1	<u>5.2</u>	4.2
H	0.0	1.9	1.3	<u>5.2</u>	3.9	1.9	3.9	0.0	3.0	0.8	4.5	9.0	0.0	0.0	4.7	3.1	5.8
I	0.0	0.0	1.3	0.0	0.0	3.9	0.6	0.0	0.0	0.0	0.0	2.3	0.0	63.9	0.0	<u>5.2</u>	3.7
K	0.0	3.9	3.9	1.9	1.9	0.6	<u>7.8</u>	0.0	11.3	0.0	3.0	<u>9.0</u>	0.0	2.1	2.1	9.9	3.7
L	0.0	8.4	4.5	0.0	1.3	3.9	3.9	0.0	1.5	0.0	1.5	4.5	0.0	<u>11.0</u>	<u>5.2</u>	12.0	3.1
M	0.0	0.6	0.6	0.0	1.3	0.6	1.9	0.0	0.0	0.0	0.0	0.8	0.0	0.0	0.5	3.1	1.6
N	0.0	1.9	0.6	13.6	1.3	0.0	1.9	0.0	<u>5.3</u>	51.9	5.3	3.8	0.0	0.0	<u>5.2</u>	4.2	2.6
P	0.0	10.4	33.8	1.3	0.0	0.0	9.7	0.0	4.5	0.0	0.0	0.0	0.0	0.0	45.5	7.3	2.1
Q	0.0	10.4	2.6	1.9	30.5	0.6	21.4	0.0	5.3	0.8	2.3	9.8	0.0	0.0	2.6	5.8	4.7
R	0.0	7.1	3.2	3.2	1.3	0.6	18.2	0.0	<u>7.5</u>	0.8	4.5	32.3	0.0	0.0	1.0	<u>9.4</u>	11.5
S	0.0	18.8	11.7	16.2	3.9	0.6	9.7	0.0	15.0	25.6	3.0	3.0	0.0	0.0	14.7	10.5	20.4
T	0.0	<u>5.2</u>	2.6	<u>5.8</u>	3.2	1.3	<u>7.8</u>	0.0	2.3	<u>6.0</u>	0.8	<u>6.0</u>	0.0	1.6	2.6	0.5	<u>5.8</u>
V	0.0	0.6	1.9	0.6	0.0	0.6	1.3	0.0	2.3	0.8	0.0	3.0	0.0	<u>17.3</u>	0.5	3.1	2.6
W	0.0	0.0	0.6	1.9	0.0	1.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.5	0.0	2.6
Y	0.0	0.0	0.6	2.6	<u>5.8</u>	5.2	0.0	0.0	0.8	0.8	0.0	0.0	0.5	2.6	1.0	2.1	1.6
	100.0	85.7	67.5	76.6	73.4	81.2	81.8	100.0	81.2	94.0	77.4	75.9	99.5	92.1	70.7	80.1	60.2
	1	9	4	6	3	2	7	1	8	4	2	6	1	3	4	10	6
	100.0	73.4	67.5	65.6	67.5	76.0	66.2	100.0	68.4	77.4	72.2	60.9	99.5	63.9	60.2	60.2	59.2
	1	7	4	4	2	1	5	1	6	2	1	4	1	1	2	7	6

FIG. 9B

18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35
1.6	2.6	0.0	0.0	1.0	2.5	5.6	0.0	0.0	6.9	0.0	4.6	4.6	0.0	0.0	16.0	3.8	0.0
0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100.0
1.0	0.0	0.0	81.2	1.5	28.4	22.3	86.3	0.0	3.8	89.3	1.5	0.0	100.0	0.0	6.9	21.4	0.0
1.0	1.6	0.0	0.0	2.0	15.7	4.6	3.6	0.0	9.9	0.0	2.3	6.9	0.0	100.0	16.8	0.8	0.0
7.9	0.5	0.0	0.0	0.5	4.6	3.0	0.0	0.0	0.0	0.0	0.8	0.0	0.0	0.0	1.5	0.8	0.0
1.0	0.0	0.0	0.0	66.0	0.5	0.0	0.0	0.0	30.5	1.5	48.9	1.5	0.0	0.0	0.8	22.9	0.0
0.0	2.6	0.0	0.0	3.6	4.1	1.5	3.6	0.0	0.8	0.8	2.3	0.0	0.0	0.0	2.3	6.1	0.0
0.0	4.7	0.0	0.0	0.0	4.6	2.0	0.0	0.0	1.5	0.0	0.0	0.0	0.0	0.0	3.1	0.8	0.0
6.8	12.6	0.0	0.0	1.0	2.5	5.1	0.0	0.0	6.1	0.0	3.8	0.0	0.0	0.0	12.2	0.8	0.0
14.7	15.2	0.0	0.0	1.5	2.0	3.0	0.0	0.0	6.9	0.0	1.5	0.8	0.0	0.0	9.9	0.8	0.0
0.5	1.0	0.0	0.0	1.5	1.0	0.0	0.0	0.0	1.5	0.0	3.1	0.8	0.0	0.0	1.5	0.8	0.0
2.1	0.0	0.0	18.8	3.6	2.0	21.3	4.1	0.0	0.0	4.6	14.5	0.0	0.0	0.0	1.5	33.6	0.0
0.0	0.5	0.0	0.0	0.0	0.0	10.7	0.0	0.0	9.9	0.0	0.0	0.0	0.0	0.0	0.0	0.8	0.0
5.8	7.3	0.0	0.0	4.1	10.7	4.6	1.5	0.0	5.3	0.8	3.1	0.0	0.0	0.0	6.1	0.8	0.0
3.7	24.1	0.0	0.0	5.6	2.5	6.1	0.0	0.0	3.8	0.0	2.3	3.1	0.0	0.0	10.7	1.5	0.0
1.0	0.0	0.0	0.0	3.0	2.0	2.0	0.5	0.0	7.6	1.5	4.6	80.9	0.0	0.0	0.8	4.6	0.0
0.5	2.6	0.0	0.0	2.5	1.5	2.0	0.5	0.0	0.8	0.8	0.0	1.5	0.0	0.0	2.3	0.0	0.0
1.0	21.5	0.0	0.0	0.5	10.2	3.6	0.0	0.0	4.6	0.0	0.0	0.0	0.0	0.0	6.1	0.0	0.0
46.6	2.6	0.0	0.0	0.5	2.0	1.5	0.0	0.0	0.0	0.0	3.1	0.0	0.0	0.0	0.8	0.0	0.0
4.7	0.5	0.0	0.0	1.5	3.0	1.0	0.0	0.0	0.0	0.8	3.8	0.0	0.0	0.0	0.8	0.0	0.0
81.7	80.6	100.0	100.0	71.6	65.0	71.1	86.3	100.0	83.2	89.3	63.4	87.8	100.0	100.0	84.7	84.0	100.0
5	5	1	2	2	4	6	1	1	8	1	2	2	1	1	8	4	1
61.3	60.7	100.0	81.2	66.0	65.0	60.4	86.3	100.0	64.1	89.3	63.4	80.9	100.0	100.0	61.1	77.9	100.0
2	3	1	1	1	4	4	1	1	5	1	2	1	1	1	5	3	1

# Figure 10

	a	b c	de	f ghi	jk lm	nop	q
IDD_HUMAN	C.....	NPGQFACRSGTIQ.....	CIPLPWQ.CDGWATCEDE.....	SDEAN.....	C		
LRP3_HUMAN	C.....	QADEFRCDNGK.....	CLPGPWQ.CNTVDECGDG.....	SDEGN.....	C		
LRP3_HUMAN	C.....	PGGTFFPCSGARSTR.....	CLPVERR.CDGLQDCGDG.....	SDEAG.....	C		
LRP3_HUMAN	C.....	LPWEQPCGSSSDSDGSLGDQGC	CFSEPQR.CDGWWHCASG.....	RDEQG.....	C		
LRP3_HUMAN	C.....	PPDQYPCEGGSSGL.....	CYTPADR.CNNQKSCPDG.....	ADEKN.....	C		
LRP3_HUMAN	C.....	QPGTFHCGTNL.....	CIFETWR.CDGQEDCQDG.....	SDEHG.....	C		
LRP5_HUMAN	C.....	SPDQFACATGEID.....	CIPGAWR.CDGFPEDDDQ.....	SDEEG.....	C		
LRP5_HUMAN	C.....	SAAQFPCARGQ.....	CVDLRLR.CDGEADCQDR.....	SDEVD.....	C		
LRP5_HUMAN	C.....	LPNQFRCASGQ.....	CVLIKQQ.CDSFPDCIDG.....	SDELM.....	C		
LRP6_HUMAN	C.....	SPQQFTCFTGEID.....	CIPVAWR.CDGFTCEDH.....	SDELN.....	C		
LRP6_HUMAN	C.....	SESQFQCASGQ.....	CIDGALR.CNGDANCQDK.....	SDEKN.....	C		
LRP6_HUMAN	C.....	LIDQFRCANGQ.....	CIGKHHK.CDHNVDCCSDK.....	SDELD.....	C		
ST7_HUMAN	C.....	ACDQFRCGNGK.....	CIPPAWK.CNNMDECGDS.....	SDEEI.....	C		
ST7_HUMAN	C.....	AYNQFQCLSRFTKVYT.....	CLPESLK.CDGNIDCLDL.....	GDEID.....	C		
ST7_HUMAN	C.....	LPWEIPCGGNWG.....	CYTEQQR.CDGYWHCPNG.....	RDETN.....	C		
ST7_HUMAN	C.....	QKEEFPCSRNGV.....	CYPRSDR.CNYQNHCPNG.....	SDEKN.....	C		
ST7_HUMAN	C.....	QPGNFHCKNNR.....	CVFESWV.CDSQDDCGDG.....	SDEEN.....	C		
CORI_HUMAN	C.....	GRGENFLCASGI.....	CIPGKLQ.CNGYNDCCDW.....	SDEAH.....	C		
CORI_HUMAN	C.....	SENLFHCHTGK.....	CLNYSLV.CDGYDDCGDL.....	SDEQN.....	C		
CORI_HUMAN	C.....	NPTTEHRCGDGR.....	CIAMEWV.CDGDHDCVVK.....	SDEVN.....	C		
CORI_HUMAN	C.....	HSQGLVECRNGQ.....	CIPSTFQ.CDGEDDCKDG.....	SDEEN.....	C		
CORI_HUMAN	C.....	SPSHFKCRSGQ.....	CVLASRR.CDGQADCDD.....	SDEEN.....	C		
CORI_HUMAN	C.....	KERDLWECPSNKQ.....	CLKHTVI.CDGFDPDCPDY.....	MDEKN.....	C		
CORI_HUMAN	C.....	QDDELECANHA.....	CVSRDLW.CDGEADCSDS.....	SDEWD.....	C		
TMS2_HUMAN	C.....	SNSGIECDSSGT.....	CINPSNW.CDGVSHCPGG.....	EDENR.....	C		
TMS3_HUMAN	C.....	SGKYRCRSSFK.....	CIELIAR.CDGVSDCKDG.....	EDEYR.....	C		
MAT_HUMAN	C.....	PGQFTCRGTGR.....	CIRKELR.CDGWADCTDH.....	SDELN.....	C		
MAT_HUMAN	C.....	DAGHQFTCKNKF.....	CKPLFWV.CDSVNDCCGN.....	SDEQG.....	C		
MAT_HUMAN	C.....	PAQTFRCNSGK.....	CLSKSQQ.CNGKDDCGDG.....	SDEAS.....	C		
MAT_HUMAN	C.....	TKHTYRCLNGL.....	CLSKGNPECCKEDCSDG.....	SDEKD.....	C		
ENTK_HUMAN	C.....	LPGSSPCTDALT.....	CIKADLF.CDGEVNCPDG.....	SDEDNKM.....	C		
ENTK_HUMAN	C.....	KADHFQCKNGE.....	CVPLVNL.CDGLHCEDE.....	SDEAD.....	C		
HAI1_HUMAN	C.....	QPTQFRCNSGC.....	CIDSFLE.CDDTPNCPDA.....	SDEAA.....	C		
CFAI_HUMAN	C.....	YTQKADSPMDFFQCVNGK.....	YISQMK.A.CDGINDCGDQ.....	SDEL.....	C		
CFAI_HUMAN	C.....	QKGKFHCKSGV.....	CIPSQYQ.CNGEVDCITG.....	EDEVG.....	C		
CO6_HUMAN	C.....	KNKFRCDSGR.....	CIARKLE.CNGENDCGDN.....	SDERD.....	C		
CO7_HUMAN	C.....	GERFRCFSGQ.....	CISKSLV.CNGDSDCDEDS.....	ADEDR.....	C		
CO8A_HUMAN	C.....	GQDFQCKETGR.....	CLKRHLV.CNGDQDCLDG.....	SDEDD.....	C		
CO8B_HUMAN	C.....	EGFVCAQTGR.....	CVNRRLL.CNGDNDCCDG.....	SDEAN.....	C		
CO9_HUMAN	C.....	GNDFQCSTGR.....	CIKMRLR.CNGDNDCCGDF.....	SDEDD.....	C		
PERL_HUMAN	C.....	TEAEFACHSYNE.....	CVALEYR.CDRRPDCRDM.....	SDELN.....	C		
PERL_HUMAN	C.....	GPQEAACRNHG.....	CIPRDYL.CDGQEDCEDG.....	SDELD.....	C		
PERL_HUMAN	C.....	EPNEFFPCGNHG.....	CALKLWR.CDGFDFCEDR.....	TDEAN.....	C		
PERL_HUMAN	C.....	GPTQFRCVSTNM.....	CIPASFH.CDEESDCPDR.....	SDEFG.....	C		
SORL_HUMAN	C.....	LRNQYRCNSGN.....	CINSIWW.CDFDNDCCGM.....	SDERN.....	C		
SORL_HUMAN	C.....	DLDTQFRCQESGT.....	CIPLSYK.CDLEDDCGDN.....	SDESH.....	C		
SORL_HUMAN	C.....	RSDEYNCSSGM.....	CIRSSWV.CDGDNDCCRDW.....	SDEAN.....	C		
SORL_HUMAN	C.....	EASNFOCRNGH.....	CIPQRAW.CDGDTCQDG.....	SDEDPVN.....	C		
SORL_HUMAN	C.....	NGFRCPNGT.....	CIPSSKH.CDGLRDCSDG.....	SDEQH.....	C		
SORL_HUMAN	C.....	THFMDFVCKNRQQ.....	CLFHSMV.CDGIIQCRDG.....	SDEDAAFAG.....	C		
SORL_HUMAN	C.....	DEFGFQCQNGV.....	CISLIWK.CDGMDDCGDY.....	SDEAN.....	C		
SORL_HUMAN	C.....	SRYFQFRCENGH.....	CIPNRWK.CDRENDCCGDW.....	SDEKD.....	C		
SORL_HUMAN	C.....	LPNYRCSSGT.....	CVMDTWV.CDGYRDCADG.....	SDEEA.....	C		
SORL_HUMAN	C.....	DRFEFECHQPKT.....	CIPNWKR.CDGHQDCQDG.....	RDEAN.....	C		
SORL_HUMAN	C.....	MSREFQCEDGEA.....	CIVLSER.CDGFLDCSDE.....	SDEKA.....	C		
APOER2_HUM	C.....	EKDQFQCRNER.....	CIPSVWR.CDEDDDCLDH.....	SDEDD.....	C		
APOER2_HUM	C.....	ADSDFTCDNGH.....	CIHERWK.CDGEEECPDG.....	SDESEAT.....	C		
APOER2_HUM	C.....	PAEKLSCGPTSHK.....	CVPASWR.CDGEKDCGG.....	ADEAG.....	C		
APOER2_HUM	C.....	APHEFQCGNRS.....	CLAAVFW.CDGDDDCGDG.....	SDEAG.....	C		
APOER2_HUM	C.....	GPREFRCGGDGGGA.....	CIPERWV.CDRQFDCEDR.....	SDEAAEL.....	C		
APOER2_HUM	C.....	ATVSQFACRSGE.....	CVHLGWR.CDGDRCCKDK.....	SDEAD.....	C		
APOER2_HUM	C.....	RGDEFQCGDGT.....	CVLAIKH.CNQEQDCPDG.....	SDEAG.....	C		
LDLR_HUMAN	C.....	ERNEFQCDGK.....	CISYKWW.CDGSAAECQDG.....	SDESQET.....	C		
LDLR_HUMAN	C.....	KSGDFSCGGRVNR.....	CIPQFWR.CDGQVDCDNG.....	SDEQG.....	C		
LDLR_HUMAN	C.....	SQDEFRCCHDGK.....	CISRQFV.CDSDRDCLDG.....	SDEAS.....	C		
LDLR_HUMAN	C.....	GPASFQCNST.....	CIPQLWA.CDNDPDCEDG.....	SDEWPQR.....	C		
LDLR_HUMAN	C.....	SAFEFHCLSGE.....	CIHSSWR.CDGGPDCKDK.....	SDEEN.....	C		
LDLR_HUMAN	C.....	RPDEFQCSNNG.....	CIHGSRQ.CDREYDCKDM.....	SDEVG.....	C		
LDLR_HUMAN	C.....	EGPNKFKCHSGE.....	CITLDKV.CNMARDCRDW.....	SDEPIKE.....	C		
LDVR_HUMAN	C.....	EPSQFQCTNGR.....	CITLLWK.CDGEDDCVDG.....	SDEKN.....	C		
LDVR_HUMAN	C.....	AESDFVCNNGQ.....	CVPSRWK.CDGDPCEDG.....	SDESPQ.....	C		

LDVR_HUMAN	C.....RIHEISCGAHSTQ.....CIPVSWR.CDGENDCDSG.....EDEEN.....C
LDVR_HUMAN	C.....SPDEFTCSSGR.....CISRNFV.CNGQDDCSDG.....SDELD.....C
LDVR_HUMAN	C.....GAHEFQCTSS.....CIPISWV.CDDADCSQ.....SDESLEQ.....C
LDVR_HUMAN	C.....PASEIQCGSGE.....CIHKKWR.CDGDPCCKDG.....SDEVN.....C
LDVR_HUMAN	C.....RPDQFECEDGS.....CIHGSQ.CNGIRDCVDG.....SDEVN.....C
LDVR_HUMAN	C.....LGPGKFCKRSGE.....CIDISKV.CNQEQDCRDW.....SDEPLKE.....C
LRP1_HUMAN	C.....SPKQFACRDQIT.....CISKGWR.CDGERDCPDG.....SDEAPEI.....C
LRP1_HUMAN	C.....QPNEHNCGLTEL.....CVPMSRL.CNGVQDCMDG.....SDEGPH.....C
LRP1_HUMAN	C.....QPGEFACANSR.....CIQERWK.CDGDNDCLDN.....SDEAPAL.....C
LRP1_HUMAN	C.....PSDRFKCENNR.....CIPNRWL.CDGDNDCGNS.....EDESAT.....C
LRP1_HUMAN	C.....PPNQFSCASGR.....CIPISWT.CDLDDDCGDR.....SDESAS.....C
LRP1_HUMAN	C.....FBLTQFTCNNGR.....CININWR.CDNDNDCGDN.....SDEAG.....C
LRP1_HUMAN	C.....SSTQFKCNSGR.....CIPEHWT.CDGDNDCGDY.....SDETHAN.....C
LRP1_HUMAN	C.....HTDEFQCRDLGL.....CIPLRWR.CDGDTCMDS.....SDEKS.....C
LRP1_HUMAN	C.....DPSVKFGCKDSAR.....CISKAWV.CDGDNDCEDN.....SDEEN.....C
LRP1_HUMAN	C.....RPPSHPCANNTSV.....CLPPDKL.CDGDNDCGDG.....SDEGEL.....C
LRP1_HUMAN	C.....RAQDEFECANGE.....CINFSLT.CDGVPCKDK.....SDEKPSY.....C
LRP1_HUMAN	C.....KKTFRCNSGR.....CVSNMLW.CNGADDCGDG.....SDEIP.....C
LRP1_HUMAN	C.....GVGEFRCRDGT.....CIGNSSR.CNQFVDCEDA.....SDEMNI.....C
LRP1_HUMAN	CSSYFRLGVKGVLFQPCERTSL.....CYAPSWV.CDGANDCGDY.....SDELD.....C
LRP1_HUMAN	C.....PLNYFACPSGR.....CIPMSWT.CDKEDDCHEG.....SDETH.....C
LRP1_HUMAN	C.....SEAQFECQNRH.....CISKQWL.CDGSDDCGDG.....SDEAAH.....C
LRP1_HUMAN	C.....GPSSFSCPGTHV.....CVPWRWL.CDGDKDCADG.....ADESIAAG.....C
LRP1_HUMAN	C.....DDREFMCQNRQ.....CIPKHFV.CDHDRDCADG.....SDESPE.....C
LRP1_HUMAN	C.....GPSEFRCANGR.....CLSSRQWECDEGNDCHDQ.....SDEAPKNPH.....C
LRP1_HUMAN	C.....NASSQFLCSSGR.....CVAEALL.CNGQDDCGDS.....SDERG.....C
LRP1_HUMAN	C.....TASQFVCKNDK.....CIPFWWK.CDTEDDCGDH.....SDEPD.....C
LRP1_HUMAN	C.....RPGQFQCSGTI.....CTNPAFI.CDGDNDCCDN.....SDEAN.....C
LRP1_HUMAN	C.....LPSQFKCTNTNR.....CIPGIFR.CNGQDNCGDG.....SDELD.....C
LRP1_HUMAN	C.....APNQFQCSITKR.....CIPRVWV.CDRDNDCCVDG.....SDEPAN.....C
LRP1_HUMAN	C.....GVDEFRCCKDSGR.....CIPARWK.CDGEDDCGDG.....SDEPKEE.....C
LRP1_HUMAN	C.....EPYQFRCKNNR.....CVPGRWQ.CDYDNDCCDN.....SDEES.....C
LRP1_HUMAN	C.....SESEFSCANGR.....CIAGRWK.CDGDHDCADG.....SDEKD.....C
LRP1_HUMAN	C.....DMDQFQCKSGH.....CIPLRWR.CDADADCMDG.....SDEEA.....C
LRP1_HUMAN	C.....PLDEFQCNNTL.....CKPLAWK.CDGEDDCGDN.....SDENPEE.....C
LRP1_HUMAN	C.....PPNRPFRCCKNDRV.....CLWIGRQ.CDGTDCNGDG.....TDEED.....C
LRP1_HUMAN	C.....KDKKEFLCRNQR.....CLSSSLR.CNMFDCCGDG.....SDEED.....C
LRP2_HUMAN	C.....DSAHFRCGSGH.....CIPADWR.CDGTKDCSD.....ADEIG.....C
LRP2_HUMAN	C.....QQGYFKCQSEGO.....CIPSSWV.CDQDQDCDDG.....SDEKQD.....C
LRP2_HUMAN	C.....SSHQITCSNGQ.....CIPSEYR.CDHVRDCPDG.....ADEND.....C
LRP2_HUMAN	C.....EQLTCDNGA.....CYNTSQK.CDWKVDCCDS.....SDEIN.....C
LRP2_HUMAN	C.....LHNEFSCNGE.....CIPRAYV.CDHNDCCQDG.....SDEHA.....C
LRP2_HUMAN	C.....GGYQFTCPSGR.....CIYQNWV.CDGEDDCKDN.....GDEEG.....C
LRP2_HUMAN	C.....SPREWSCPESGR.....CISYQVW.CDGILDCPGR.....EDENNTSTGKYC.....C
LRP2_HUMAN	C.....GLFSFPCKNGR.....CVPNYYL.CDGVDDCHDN.....SDEQL.....C
LRP2_HUMAN	C.....SSSAFTCGHGE.....CIPAHWR.CDKRNDCCVDG.....SDEHN.....C
LRP2_HUMAN	C.....LDTQYTCDNHQ.....CISKNWV.CDTDNDCCGDG.....SDEKN.....C
LRP2_HUMAN	C.....QPSQFNCPNHR.....CIDLSFV.CDGDKDCVDG.....SDEVG.....C
LRP2_HUMAN	C.....TASQFKCASGDK.....CIGVTNR.CDGVFDCSDN.....SDEAG.....C
LRP2_HUMAN	C.....HSDEFQCEQDGI.....CIPNFEW.CDGHPCCLYG.....SDEHNA.....C
LRP2_HUMAN	C.....PSSYFHCNDGN.....CIHRAWL.CDRDNDCCGDM.....SDEKD.....C
LRP2_HUMAN	C.....PSWQWQCLGHNI.....CVNLSVV.CDGIFDCPNG.....TDESPL.....C
LRP2_HUMAN	C.....GASSFTCSNGR.....CISEEWK.CDNDNDCCGDG.....SDEMSV.....C
LRP2_HUMAN	C.....SPTAFTCANGR.....CVQYSYR.CDYNDCCGDG.....SDEAG.....C
LRP2_HUMAN	C.....NATTEFMCNNRR.....CIPREFI.CNGVDNCHDNT.....SDEKN.....C
LRP2_HUMAN	C.....QSGYTKCHNSNI.....CIPRVYL.CDGDNDCCGDN.....SDENPTY.....C
LRP2_HUMAN	C.....SSSEFQCASGR.....CIPQHWY.CDQETDCFDA.....SDEPAS.....C
LRP2_HUMAN	C.....LADEFKCDGGR.....CIPSEWI.CDGDNDCCGDM.....SDEKRRHQ.....C
LRP2_HUMAN	C.....SDSEFLCVNDRPPDRR.....CIPQSWV.CDGDVDCDGT.....YDENQN.....C
LRP2_HUMAN	C.....SENEFTCGYGL.....CIPKIFR.CDRHNDCCDY.....SDERG.....C
LRP2_HUMAN	C.....QQNQFTCQNGR.....CISKTFV.CDEDNCCGDG.....SDELMHL.....C
LRP2_HUMAN	C.....PPHEFKCDNGR.....CIEMMKL.CNHLDDCLDN.....SDEKG.....C
LRP2_HUMAN	C.....SSTQFLCANNEK.....CIPWVKL.CDGQKDCSDG.....SDEAL.....C
LRP2_HUMAN	C.....RLGQFQCSGDN.....CTSPQTL.CNAHQNCPDG.....SDEDRLL.....C
LRP2_HUMAN	C.....DSNEWQCANKR.....CIPESWQ.CDTFNDCCDN.....SDESSH.....C
LRP2_HUMAN	C.....RPGQFRCANGR.....CIPQAWK.CDVDNDCCGDH.....SDEPIEE.....C
LRP2_HUMAN	C.....DNFTEFSCKTNYR.....CIPKQWV.CNGVDDCRDN.....SDEQG.....C
LRP2_HUMAN	C.....HPVGDFRCKNHH.....CIPLRWQ.CDGQNDCCGDN.....SDEEN.....C
LRP2_HUMAN	C.....TESEFRCVNQQ.....CIPSRWI.CDHYNDCCDN.....SDELD.....C
LRP2_HUMAN	C.....HPEYFQCTSGH.....CVHSELK.CDGSADCLDA.....SDEAD.....C
LRP2_HUMAN	C.....QATMFECKNHV.....CIPPYWK.CDGDDDCGDG.....SDEELHL.....C
LRP2_HUMAN	C.....NSPNRFRCDNNR.....CIYSHEV.CNGVDDCCGDG.....TDETEEH.....C
LRP2_HUMAN	C.....TEYFYKCGNGH.....CIPHDNV.CDDADDCGDW.....SDELG.....C
LR1B_HUMAN	C.....DPGEFLCHDHVT.....CVSQSWL.CDGDPCPDG.....SDESLDT.....C
LR1B_HUMAN	C.....PLNHIACLGTNK.....CVHLSQL.CNGVLDCPDG.....YDEGVH.....C
LR1B_HUMAN	C.....KAGEFRCKNRH.....CIQARWK.CDGDDDCLDG.....SDEDSVN.....C

LR1B_HUMAN	C	.....PDDQFKCQNNR	.....CIPKRWL	CDGANDCGSN	.....EDESNOT	.....C
LR1B_HUMAN	C	.....QVDQFSCGNGR	.....CIPRAWL	CDREDDCGDQ	.....TDEMAS	.....C
LR1B_HUMAN	C	.....EPLTQFVCKSGR	.....CISKWH	CDSDDDCGDG	.....SDEVG	.....C
LR1B_HUMAN	C	.....FDNQFRCSGR	.....CIPGHW	CDGDNDCGDF	.....SDEAQIN	.....C
LR1B_HUMAN	C	.....NGNEFQCHPDGN	.....CVPDLWR	CDGEKDCEDG	.....SDEKG	.....C
LR1B_HUMAN	C	.....DHKTKFSCWSTGR	.....CINKAWV	CDGDDICEDQ	.....SDEDD	.....C
LR1B_HUMAN	C	.....GPPKHPCANDTSV	.....CLQPEKL	CNGKKDCPDG	.....SDEGYL	.....C
LR1B_HUMAN	C	.....NAYSEFECNGE	.....CIDYQLT	CDGIPHCKDK	.....SDEKLLY	.....C
LR1B_HUMAN	C	.....RRGFKPCYNRR	.....CIPHGKL	CDGENDCGDN	.....SDELD	.....C
LR1B_HUMAN	C	.....ATVEFRCADGT	.....CIPRSAR	CNQNICADA	.....SDEKN	.....C
LR1B_HUMAN	C	CTHFKYKLGKTTGFIRCNSTSL	.....CVLPTWI	CDGSNDCGDY	.....SDELK	.....C
LR1B_HUMAN	C	.....EENYFSCPSGR	.....CILNTWI	CDGQKDCEDG	.....RDEFH	.....C
LR1B_HUMAN	C	.....SWNQFACSAQK	.....CISKHWI	CDGEDDCGDG	.....LDESISI	.....C
LR1B_HUMAN	C	.....AADMFSCQGSRA	.....CVPRLWL	CDGERDCPDG	.....SDELSTAG	.....C
LR1B_HUMAN	C	.....DENAFMCHNKV	.....CIPKQFV	CDHDDDCGDG	.....SDESPQ	.....C
LR1B_HUMAN	C	.....GTEEFSCADGR	.....CLLNTQWQC	CDGDFDCPDH	.....SDEAPLNPK	.....C
LR1B_HUMAN	C	.....NSSFFMCKNGR	.....CIPSGGL	CDNKDDCGDG	.....SDERN	.....C
LR1B_HUMAN	C	.....TASQFRCKTDK	.....CIPFWWK	CDTVDDCGDG	.....SDEPDD	.....C
LR1B_HUMAN	C	.....QPGRFQCGTGL	.....CALPAFI	CDGENDCGDN	.....SDELN	.....C
LR1B_HUMAN	C	.....LSGQFKCTKNQK	.....CIPVNL	CNGQDDCGDE	.....EDERD	.....C
LR1B_HUMAN	C	.....SPDYFQCKTTKH	.....CISKLWV	CDDEPDCADE	.....SDEAN	.....C
LR1B_HUMAN	C	.....GPHEFQCKNNN	.....CIPDHR	CDSQNDCCSDN	.....SDEEN	.....C
LR1B_HUMAN	C	.....TLKDFLCANGD	.....CVSSRFW	CDGDFDCADG	.....SDERN	.....C
LR1B_HUMAN	C	.....SKDQFRCSNGQ	.....CIPAKWK	CDGHEDCKYG	.....EDEKS	.....C
LR1B_HUMAN	C	.....SSREYICASDG	.....CISASLK	CNGEYDCADG	.....SDEMD	.....C
LR1B_HUMAN	C	.....KEDQFRCKNAH	.....CIPIRWL	CDGIHDCVDG	.....SDEEN	.....C
LR1B_HUMAN	C	.....RADEFLCNNSL	.....CKLHFWV	CDGEDDCGDN	.....SDEAPDM	.....C
LR1B_HUMAN	C	.....PSTRPHRCRNNRI	.....CLQSEQM	CNGIDECGDN	.....SDEDH	.....C
LR1B_HUMAN	C	.....KKDEFACSNKK	.....CIPMDLQ	CDRLDDCGDG	.....SDEQG	.....C
075851	C	.....AEGEALCQENGH	.....CVPHGWL	CDNQDDCGDG	.....SDEEGE	.....C
075851	C	.....GEGQMTCSGSH	.....CLPLALL	CDRQDDCGDG	.....TDEPSYP	.....C
075851	C	.....PQGLLACADGR	.....CLPPALL	CDGHPDCLDA	.....ADEES	.....C
075851	C	.....VPGEVSCVDGT	.....CLGAIQL	CDGVWDCPDG	.....ADEGPGH	.....C
ENSP00000262089						
= 075851	C	.....GPFEFRCGSGE	.....CTPRGWR	CDQEEDCADG	.....SDERG	.....C
ENSP00000262089						
	C	.....APHHAPCARGPH	.....CVSPEQL	CDGVRQCPDG	.....SDEGPDA	.....C
075851	C	.....PGLFPCGVAPGL	.....CLTPEQL	CDGIPDCPQG	.....EDEL	.....C
075851	C	.....PEYTCPNGT	.....CIGFQLV	CDGQPDGCRPGQVGPSPPEEQG	.....C	
075851	C	.....EPGVGLRCASGE	.....CVLRGGP	CDGVLDCEDEG	.....SDEEG	.....C
ENSP00000262089						
	C	.....GPGQTPCEVLG	.....CVEQAQV	CDGREDCLDG	.....SDERH	.....C
075851	C	.....SPSQLSCGSGE	.....CLSAERR	CDLRPDQDG	.....SDEDEG	.....C
C18ORF1	C	.....KFTCTSGK	.....CLYLGSLVCN	QQNDCGDN	.....SDEEN	.....C
AAH07083/Q9NPF0						
	C	.....PPTKFQCRTSGL	.....CVPLTWR	CDRDLDCSDG	.....SDEEE	.....C
AAH07083/Q9NPF0						
	C	.....LAGELRCTLSD	.....CIPLTWR	CDGHPDCPDS	.....SDELG	.....C
Q9HXB9	C	.....SLGYFPCGNITK	.....CLPQLLH	CNGVDDCGNQ	.....ADEDN	.....C
Q9BY79/Q96DQ9	C	.....AHDEFRCQDLI	.....CLLPDSV	CDGFANCADG	.....SDETN	.....C
Q9BY79/Q96DQ9	C	.....GPSELSCQAGG	.....CKGVQWM	CDMWRDCTDG	.....SDDN	.....C
BAB55257 =						
ENSP00000239367						
	C	.....SRYHFFCDDGC	.....CIDITLA	CDGVQQCPDG	.....SDEDF	.....C
095518 =	C	.....PGEFLCSVNGL	.....CVPA	.....CDGVKDCPNG	.....LDERN	.....C
ENSP00000255793						
ENSP00000255793						
	C	.....RATFQCKEDST	.....CISLPKV	CDGQPDCLNG	.....SDEEQ	.....C
ENSP00000255793						
	C	.....GTFTFQCEDRS	.....CVKKPNPQ	CDGRPDICRDG	.....SDEEH	.....C
Q8WXD0	C	QKGYFPCGNLTK	CLPRAF	CDGKDDCGNG	ADEEN	C
Q8NB0	C	STARYHCKNGL	CIDKSFI	CDGQNNCQDN	SDEES	C
Q8NB0	C	GPTFFPCASGIH	CIIGRFR	CNGFEDCPDG	SDEEN	C
Q8NB0	C	NIPGNFMCSNGR	CIPGAWQ	CDGLPDCFDK	SDEKE	C
MEGF7	C	ALDQFLCWNGR	CIGQRKL	CNGVNDCCDN	SDESPQQN	C
MEGF7	C	EEDFPCQNGY	CIRSLWH	CDGDNDCCDN	SDEQ	C
MEGF7	C	RSGEFMCDSGL	CINAGWR	CDGDADCDQ	SDERN	C
MEGF7	C	TAEQFRCHSGR	CVRLSWR	CDGEDDCADN	SDEEN	C
MEGF7	C	SPLDFHCDNGK	CIRRSVW	CDGDNDCCDD	SDEQD	C
MEGF7	C	NLEEFQCAAGR	CILDIYH	CDGDDDCGDW	SDESD	C
MEGF7	C	SDKEFRCSGDS	CIAEHY	CDGDTCKDG	SDEEN	C
MEGF7	C	GRSHFTCAVSALGECT	CIPAQWQ	CDGDNDCCDH	SDEDEG	C
CAD61944	C	LQEEFQCLNHR	CVSAVQR	CDGVDACGDG	SDEAG	C

CAD61944	C	PPGHFPCGAAGTSGATA	CYLPADR CNYQTFCADG	ADERR	C
CAD61944	C	QPGNFRCRDEK	CVYETWV CDGQPDCADG	SDEWD	C
ENSG00000181006	C	PEITDFLCRDKK	CIASHLL CDYKPD CSDR	SDEAH	C
ENSP00000320248	C	NNRTFKCGNDI	CFRKQNAKCDGTVD CPDG	SDEEG	C
ENSP00000277547	C	PPGHHHCQNKV	CVEPQQL CDGEDNCGDL	SDENPLT	C
ENSP00000320022	C	KQGHLACGDL	CVPPEQL CDFEEQCAGG	EDEQA	C
ENSP00000313222	C	PGNSFSCGNSQ	CVTKVNPECDDQEDCSDG	SDEAH	C

Figure 11

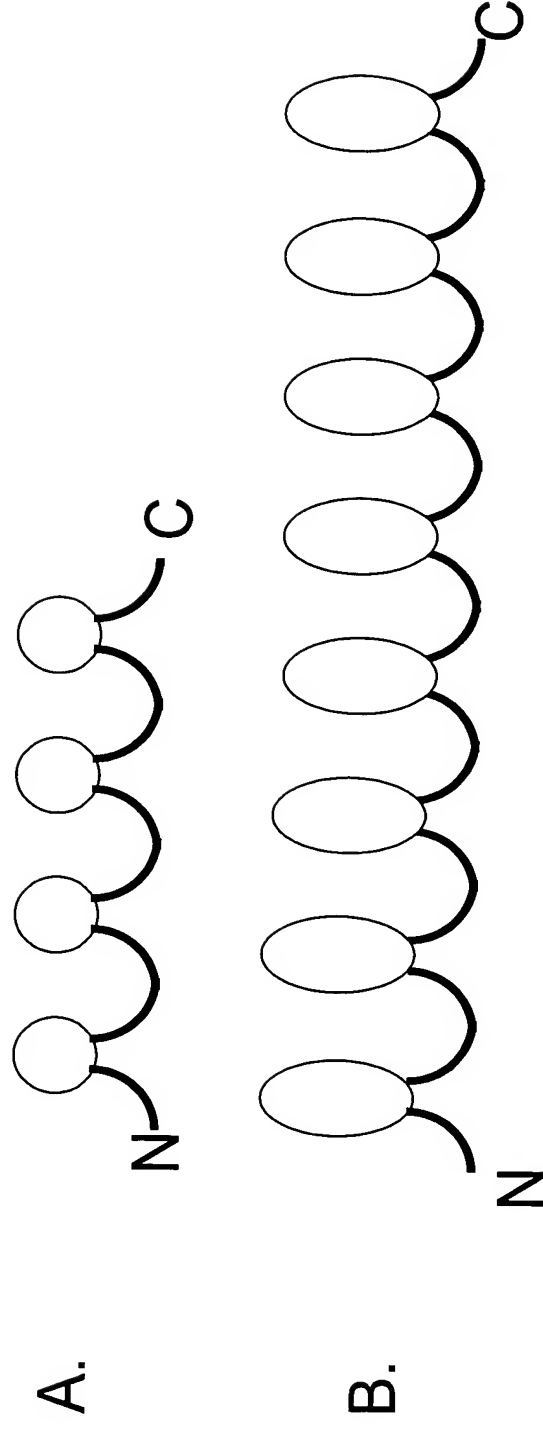
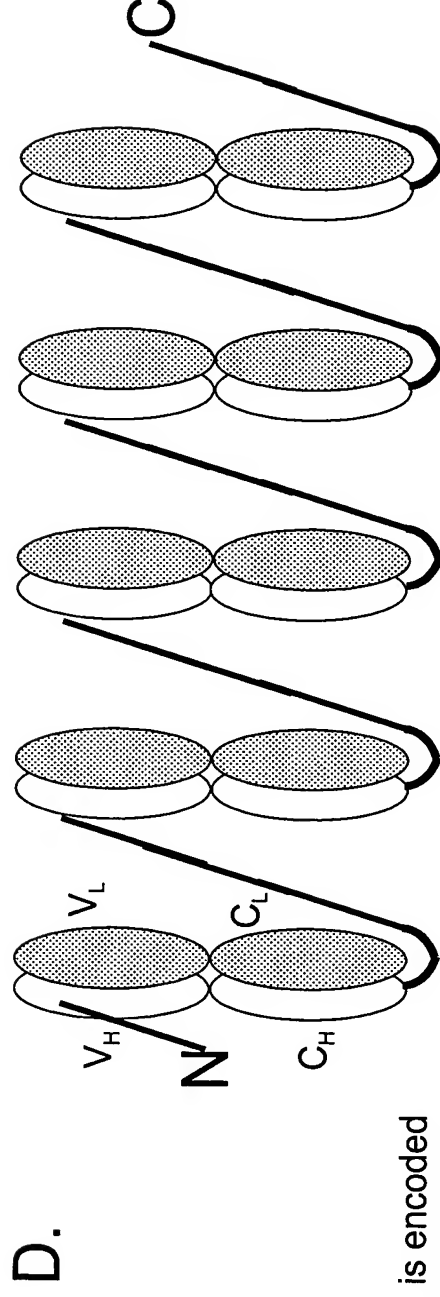
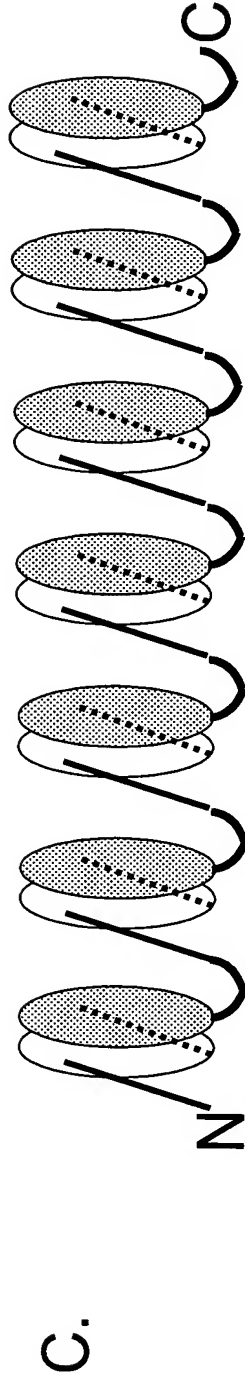


Figure 11



Light chain is encoded  
as a separate protein

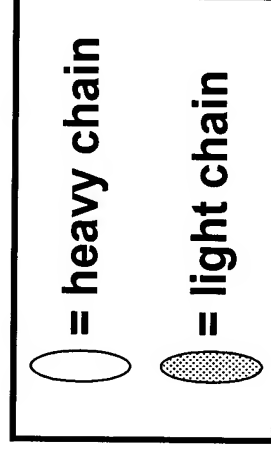
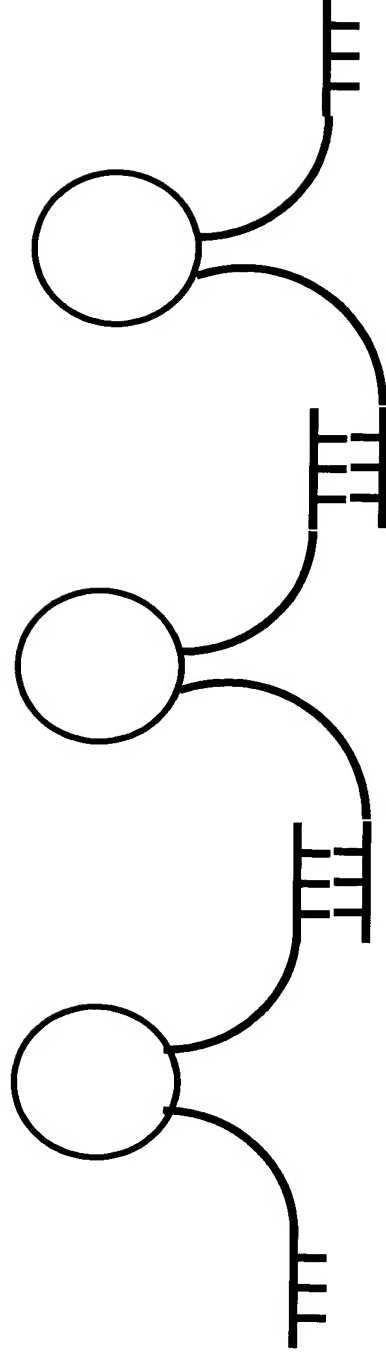




Figure 12

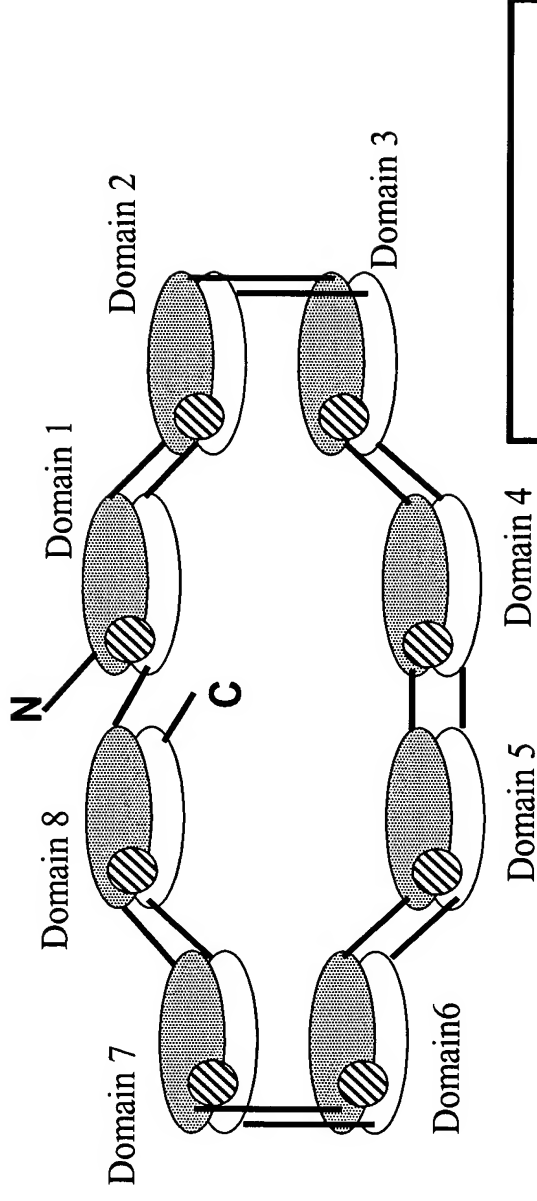


○ = any monomer domain  
▄▄▄ = obligate heterodimeric linker

Figure 13

A.

One Chain  
Multimer of  
Fv's



B.

Two Chain  
Multimer of  
Fv's

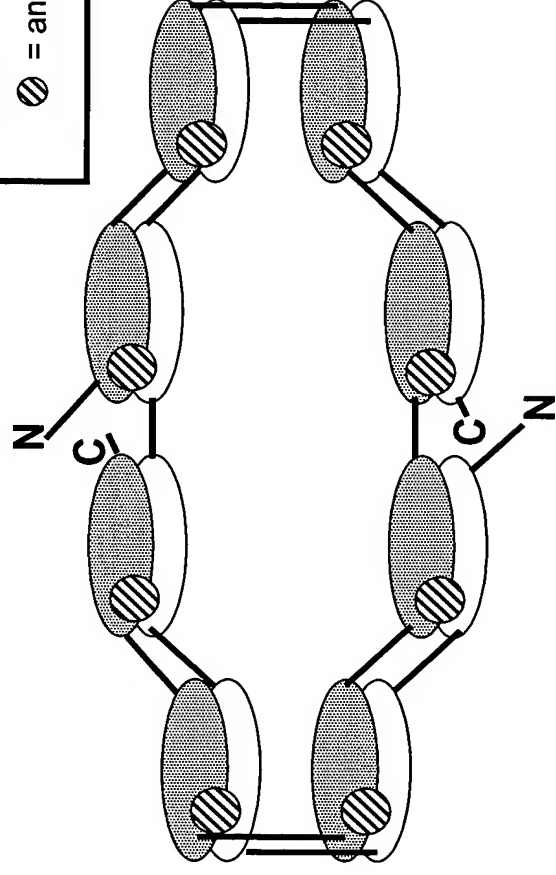


Figure 13C

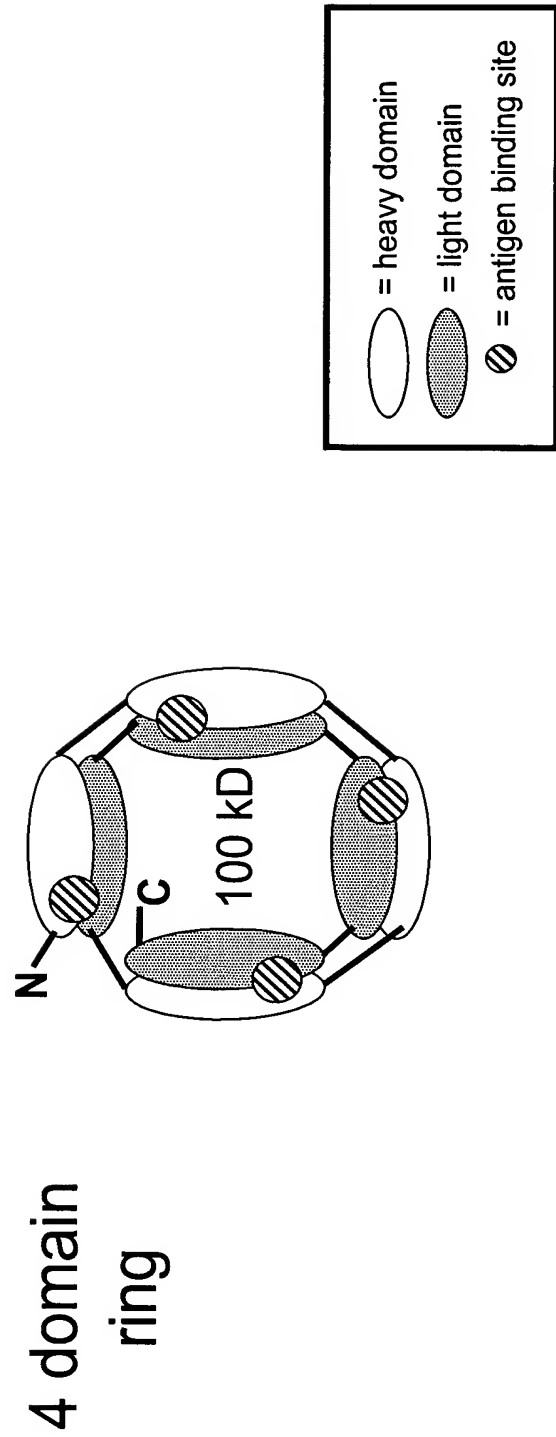
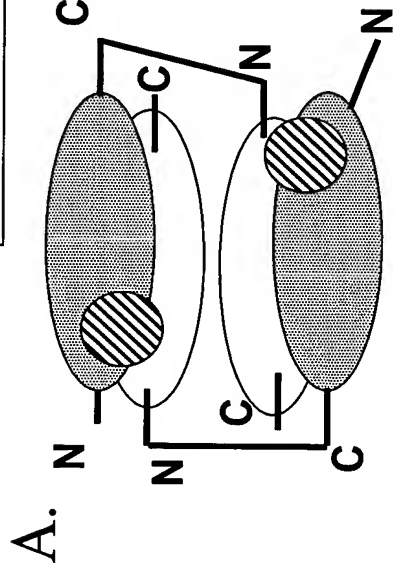
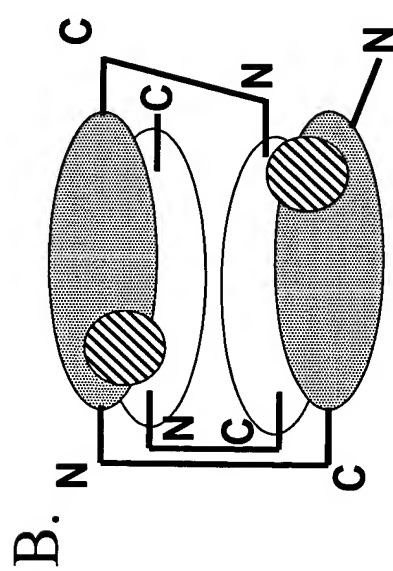
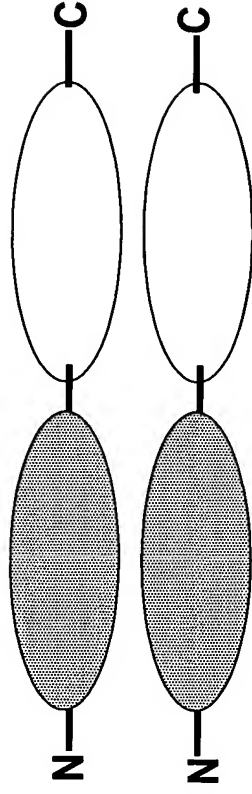


Figure 14



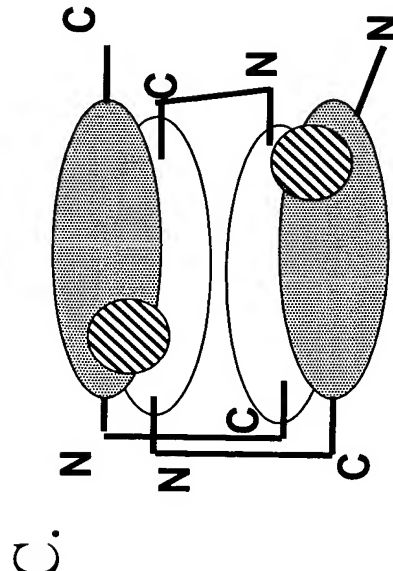
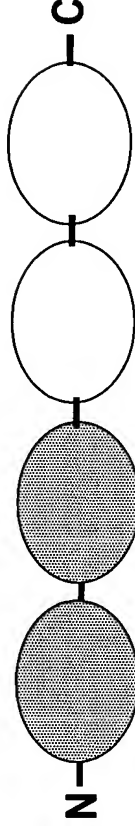
2 chain, 2 Fv  
multimer

↓



Single chain  
multimer

↓



Single chain  
multimer

↓

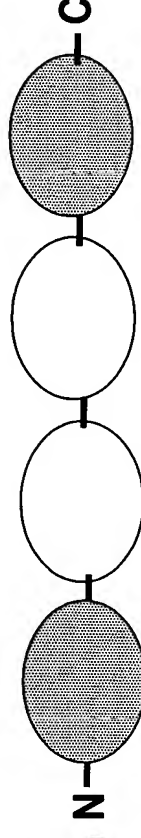
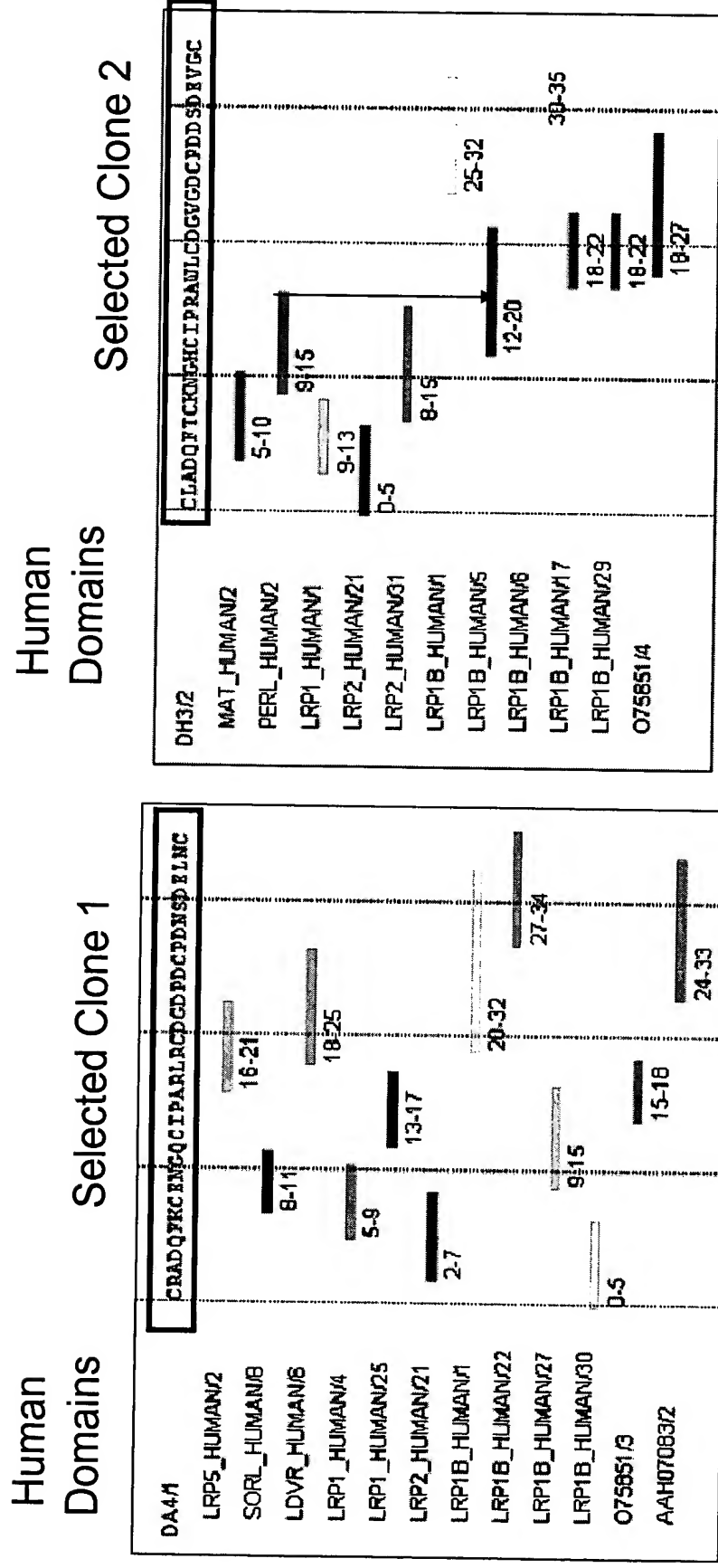
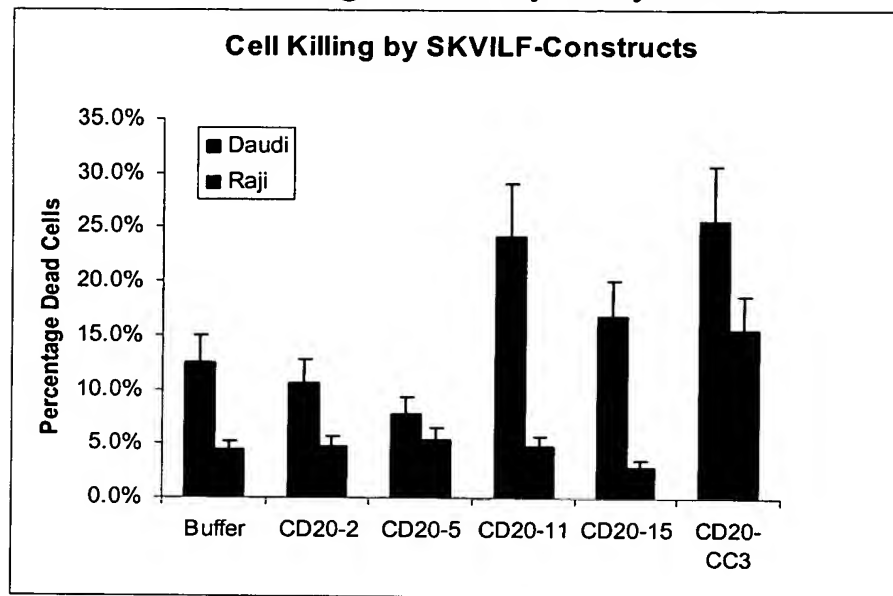


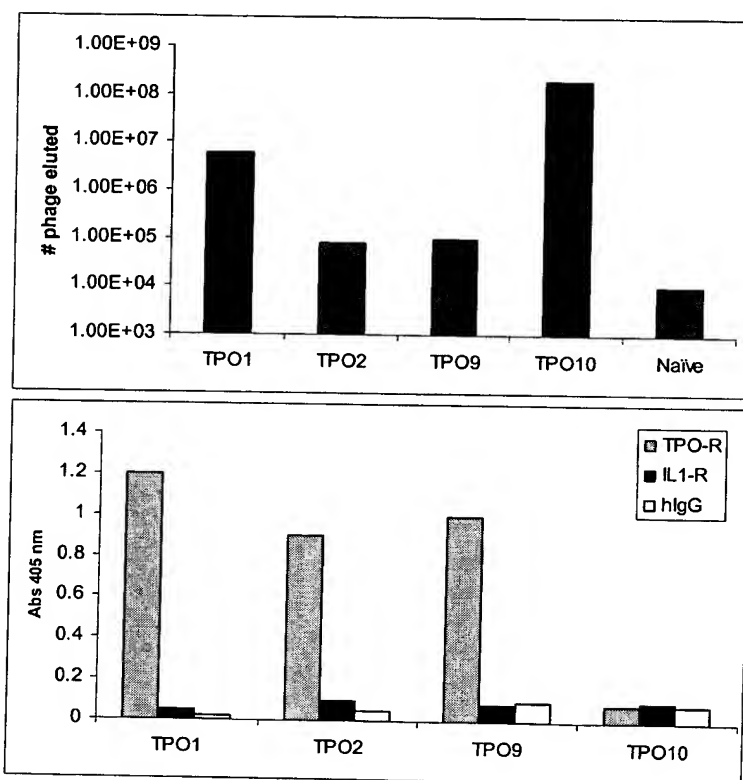
Figure 15



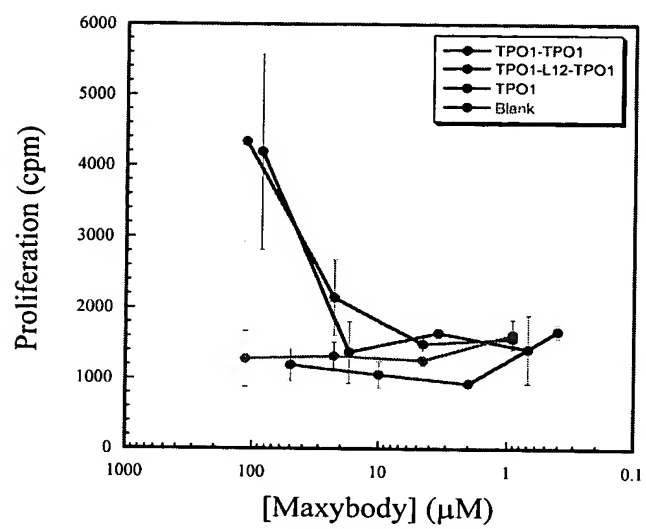
**Figure 16**  
**Cell Killing induced by Maxybodies**



**Figure 17: TPO-R Phage Specificity Data**

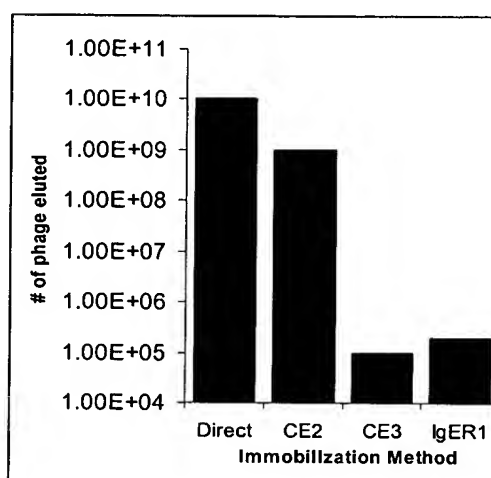


**Figure 18: TF1 Proliferation Assay**





**Figure 19 : Epitope mapping of IgE-Binding Monomer**



**Figure 20**

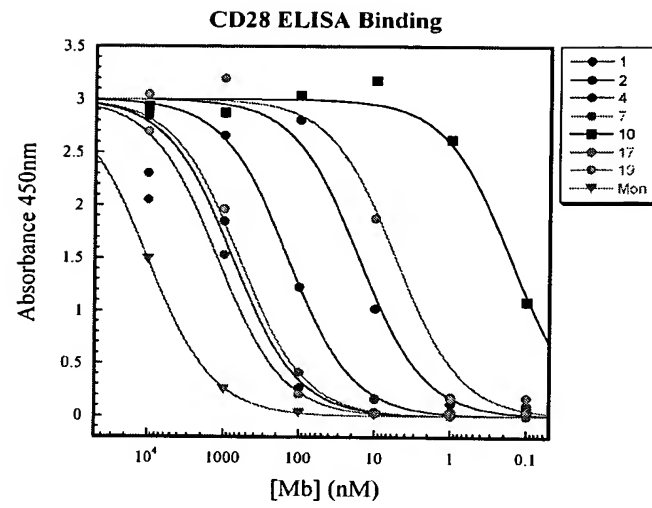


Figure 21

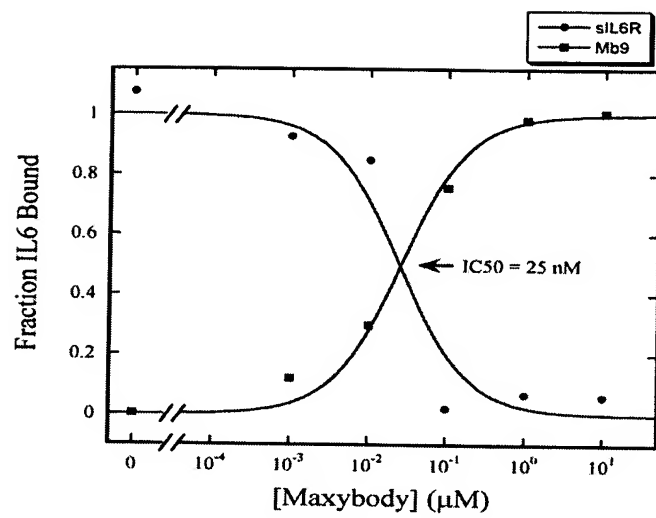
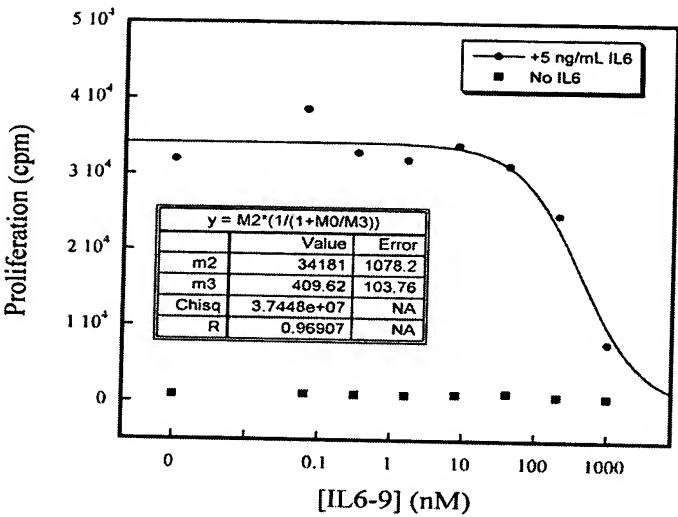


Figure 22



**Figure 23**

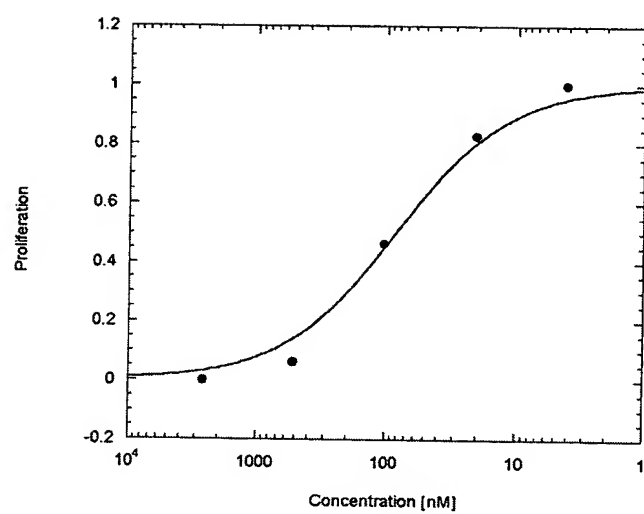
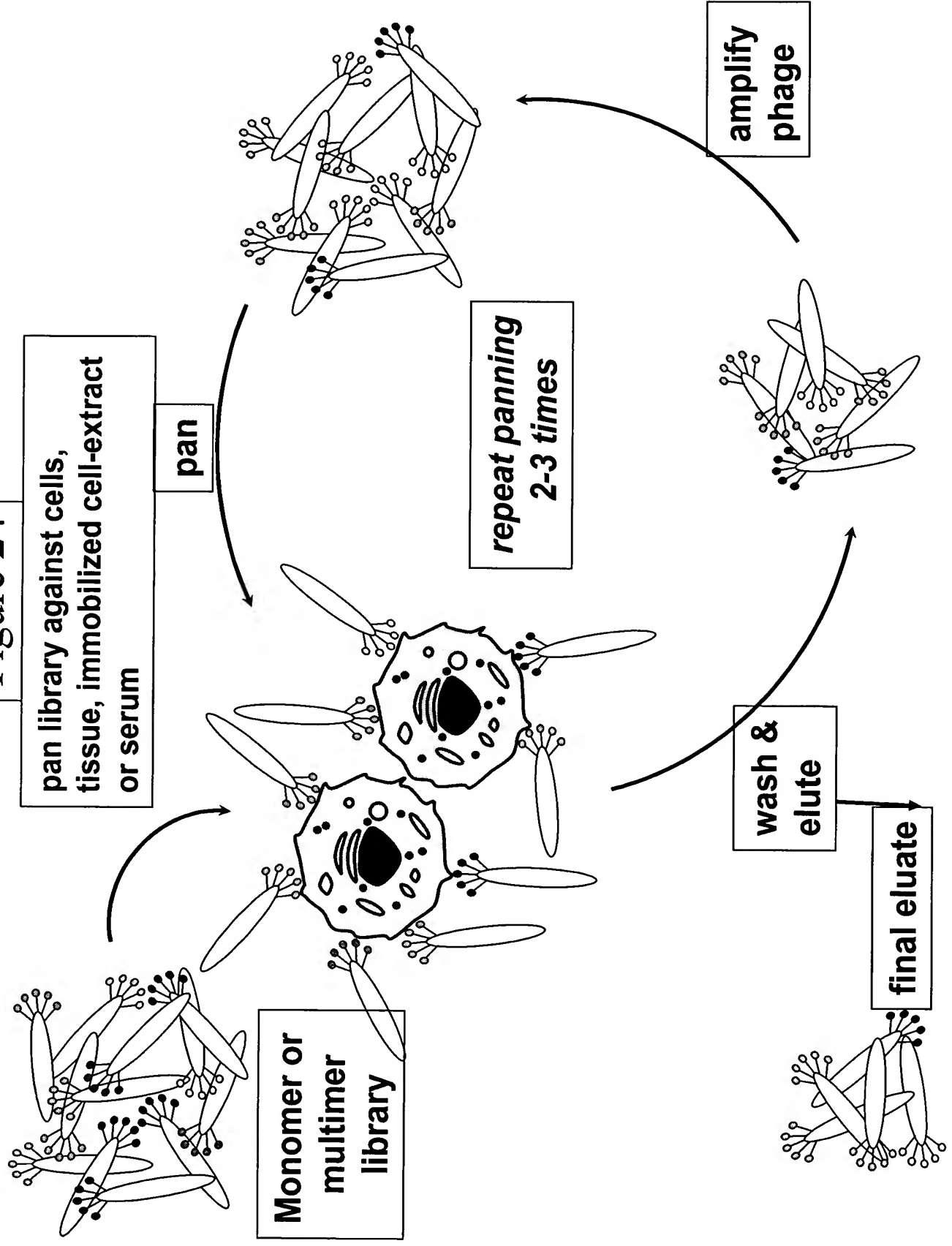


Figure 24



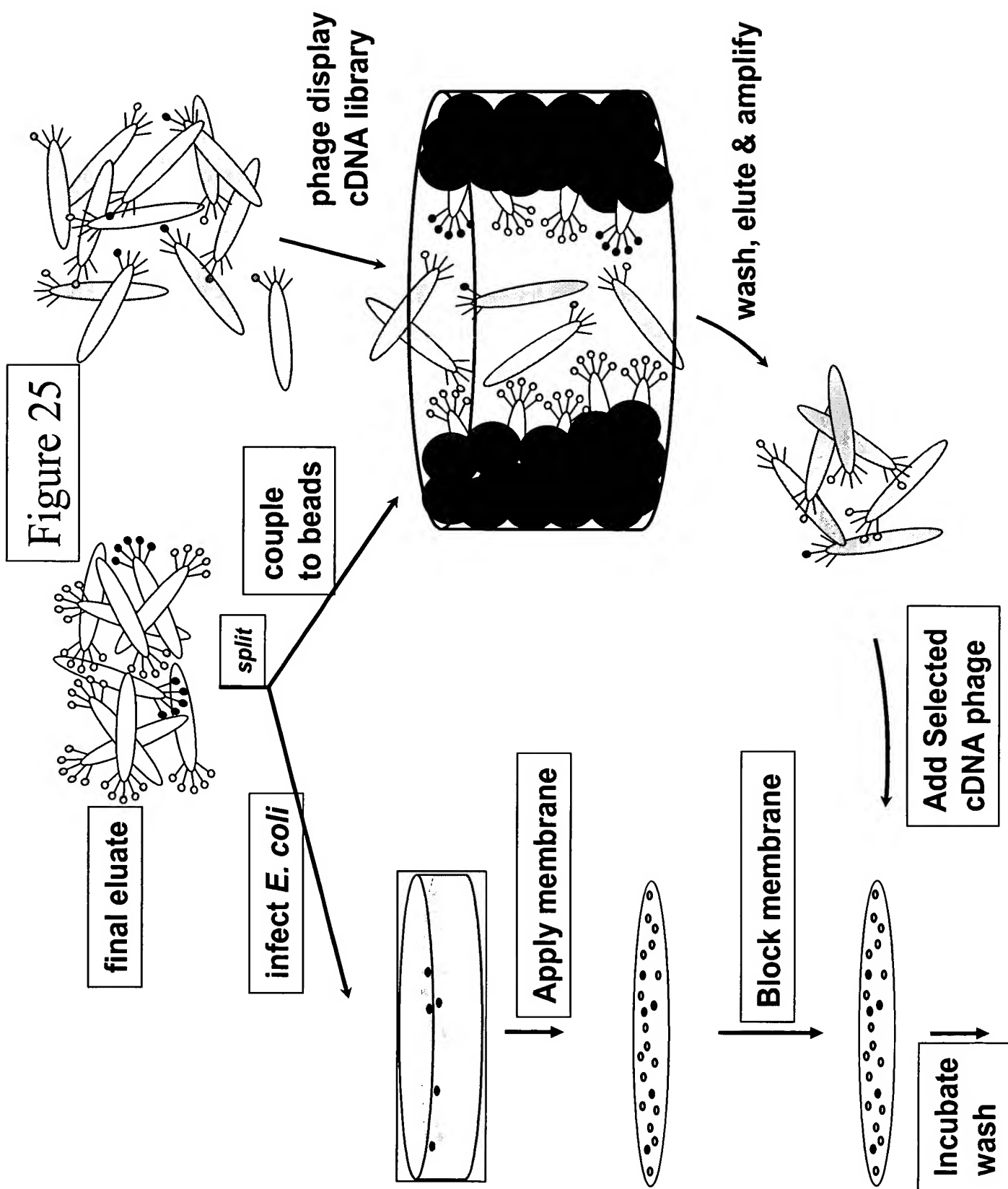
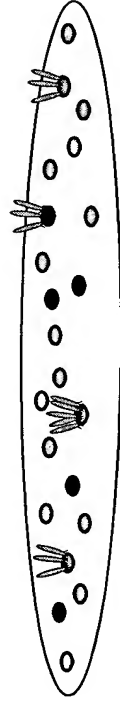
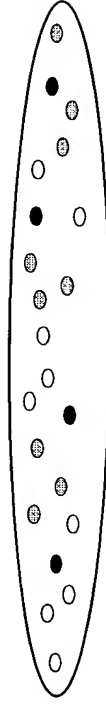


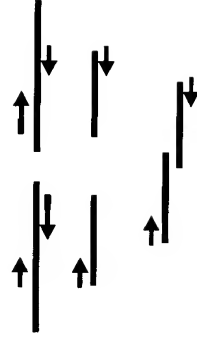
Figure 26



Stain membrane using cDNA phage specific MAb (HRP labeled)  
Add substrate



Cut positive spots out of membrane and add to PCR tube  
PCR amplify cDNA and MB sequences



Sequence PCR fragments



Figure 27

Format Variations

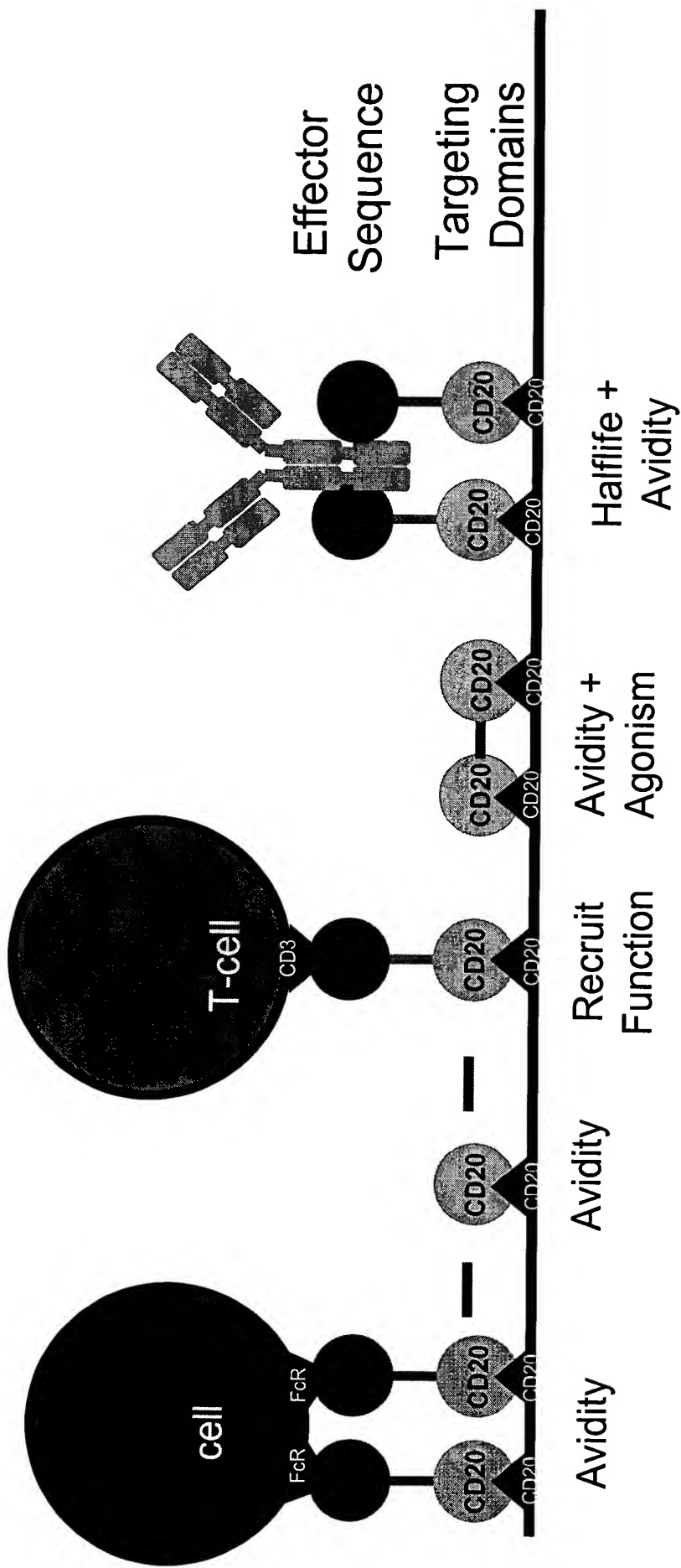
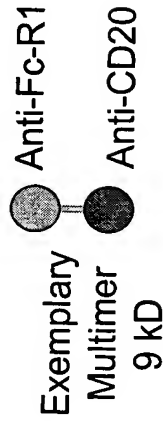


Figure 28

## Multimer Format



Monovalent Binding

Complex Stabilization

